

GenCore version 5.1.4-P5_4578
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OM protein - protein search, using sw model

Run on: March 20, 2003, 04:42:36 ; Search time 70 Seconds
(without alignments)
459.191 Million cell updates/sec

Title: US-09-867-958-1

Perfect score: 849
Sequence: 1 MAQHARTLWYDRPMVFMF.....PPAMDIDDDSDSDATSN 156

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	685	80.7	525	4	Q9BTE6
2	645	76.0	131	11	Q9P9A7
3	642	75.6	140	11	Q9D0U4
4	340.5	40.1	160	11	Q9D0V0
5	325.5	38.3	241	11	Q9CRH1
6	148	17.4	179	10	Q9FR34
7	131.5	15.5	178	10	Q9FR62
8	125	14.7	371	5	Q9VUX8
9	125	14.7	371	5	Q8STI0
10	122	14.4	190	11	Q09003
11	121	14.3	241	10	Q9FT78
12	121	14.3	262	10	Q81288
13	117	13.8	216	3	Q8X041
14	115	13.5	362	4	Q96T12
15	115	13.5	370	4	Q9N0A7
16	115	13.5	373	4	Q9P035

17	89.5	10.5	305	4	Q9BTE6	Q9BTE6
18	89.5	10.5	484	4	Q13793	Q9BTE6
19	89.5	10.5	547	4	Q13764	Q9BTE6
20	89.5	10.5	695	6	Q9SKN7	Q9BTE6
21	88	10.4	408	10	Q9MAR4	Q9BTE6
22	88	10.4	848	16	Q9TRK7	Q9BTE6
23	84.5	10.0	396	3	Q9USQ4	Q9BTE6
24	84.5	10.0	678	5	Q9V306	Q9BTE6
25	84	9.9	770	6	Q9RTU0	Q9BTE6
26	83.5	9.8	695	11	Q60496	Q9BTE6
27	83.5	9.8	695	11	P97487	Q9BTE6
28	82.5	9.7	389	10	Q48706	Q9BTE6
29	82.5	9.7	803	4	Q9P2W4	Q9BTE6
30	82.5	9.7	1226	4	Q9NZ86	Q9BTE6
31	82	9.7	297	10	Q9M4T5	Q9BTE6
32	82	9.7	345	11	Q9JHR8	Q9BTE6
33	82	9.7	839	16	Q97F94	Q9BTE6
34	82	9.7	4368	5	Q61851	Q9BTE6
35	81.5	9.6	1430	5	Q23541	Q9BTE6
36	81	9.5	683	5	Q903G8	Q9BTE6
37	80	9.4	382	3	Q13782	Q9BTE6
38	80	9.4	512	2	Q45372	Q9BTE6
39	79	9.3	364	11	Q9DJM3	Q9BTE6
40	78.5	9.2	407	5	Q9N6J0	Q9BTE6
41	78.5	9.2	407	5	Q9N6A1	Q9BTE6
42	78.5	9.2	407	5	Q9N6A1	Q9BTE6
43	78.5	9.2	817	12	Q90761	Q9BTE6
44	78.5	9.2	817	12	Q9J5H1	Q9BTE6
45	77	9.1	593	5	Q97226	Q9BTE6

ALIGNMENTS

RESULT 1

Q9BTE6 PRELIMINARY; PRT: 525 AA.

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Hypothetical 58.8 kDa protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LUNG;

RA Strausberg R.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC004172; AAH04172.1; -

DR EMBL; BC019324; AAH19324.1; -

DR InterPro; IPR002318; trna-synt_2c.

KW Hypothetical protein

SQ SEQUENCE 525 AA; 58752 MW; 04F376DFD308BC68 CRC64;

Query Match 80.7%; Score 685; DB 4; Length 525;

Best Local Similarity 100.0%; Pred. No. 2.8e-57;

Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 MEFEVVESTDVHYLIEDHRIYVSCKNADGVELYNEIEFYAVKNSKDSQDRSSRSITCFV 78

DB 1 MEFEVVESTDVHYLIEDHRIYVSCKNADGVELYNEIEFYAVKNSKDSQDRSSRSITCFV 60

QY 79 RKMEKXAMPRLTKEDIKPWLSTVDPDNWRMEDEDEMLAHVHYALLKYSIKRPP 138

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Db      61 RKKMKEXAMPRLTKEDIKPVWLSVDFPNWRMDEGDEEMELAHVEHYAELLKKVSTKRP 120
OY      139 AMDDL 144
        |||||
Db      121 AMDDL 126

RESULT 2
OY9DA7 09DA7 PRELIMINARY; PRT; 131 AA.
AC      09DA7;
DT      01-JUN-2001 (TREMblrel. 17, Created)
DT      01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT      01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE      1700113122RIK protein.
GN      1700113122RIK.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=TESTIS;
RX      MEDLINE=21085660; PubMed=11217851;
RA      Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA      Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA      Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA      Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA      Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA      Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA      Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA      Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA      Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA      Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA      Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA      Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA      Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P.,
RA      Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA      Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA      Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA      Wyszew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlski S.,
RA      Hayashizaki Y.,
RT      "Functional annotation of a full-length mouse cDNA collection."
RL      Nature 409:685-690(2001).
DR      EMBL: AK007198; BAB24896.1;
DR      MGD: MGI:1920885; 1700113122RIK.
SQ      SEQUENCE 131 AA; 15652 MW; 08DD8BAAD081823 CRC64;

Query Match      76.0%; Score 645; DB 11; Length 131;
Best Local Similarity 80.5%; Pred. No. 3.5e-54;
Matches 120; Conservative 4; Mismatches 7; Indels 18; Gaps 1;

OY      1 MARQARTLWDRPMYVMEFCVEDSTDVHVLIEDHRIYFSCKNNDGVLNIEIFYAKV 60
Db      1 MERQARTLWDRPMYVMEFCVEDSTDVHVLIEDHRIYFSCKNNDGVLNIEIFYAKV 60
OY      61 NSKDSQDRSSRSTICFVKKMKEXAMPRLTKEDIKPVWLSVDFPNWRMDEGDEEMELAH 120
Db      61 NSKDSQDRSSRSTICFVKKMKEXAMPRLTKEDIKPVWLSVDFPNWRMDEGDEEMELAH 120
OY      121 VEHYAELLKKVSTKRPAMDLDSDS 149
Db      121 VEHYAEL-----DDSDS 131

RESULT 3
OY9D0U4 09D0U4 PRELIMINARY; PRT; 140 AA.
AC      09D0U4;
DT      01-JUN-2001 (TREMblrel. 17, Created)
DT      01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT      01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE      1110069E20RIK protein.

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GN      1110069E20RIK.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX      MEDLINE=21085660; PubMed=11217851;
RA      Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA      Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA      Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA      Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA      Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA      Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA      Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA      Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA      Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA      Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA      Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA      Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA      Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P.,
RA      Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA      Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA      Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA      Wyszew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlski S.,
RA      Hayashizaki Y.,
RT      "Functional annotation of a full-length mouse cDNA collection."
RL      Nature 409:685-690(2001).
DR      EMBL: AK004415; BAB23297.1;
DR      MGD: MGI:1916146; 1110069E20RIK.
SQ      SEQUENCE 140 AA; 16849 MW; 669494AA3F63A967 CRC64;

Query Match      75.6%; Score 642; DB 11; Length 140;
Best Local Similarity 88.0%; Pred. No. 7.3e-54;
Matches 117; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

OY      1 MARQARTLWDRPMYVMEFCVEDSTDVHVLIEDHRIYFSCKNNDGVLNIEIFYAKV 60
Db      1 MERQARTLWDRPMYVMEFCVEDSTDVHVLIEDHRIYFSCKNNDGVLNIEIFYAKV 60
OY      61 NSKDSQDRSSRSTICFVKKMKEXAMPRLTKEDIKPVWLSVDFPNWRMDEGDEEMELAH 120
Db      61 NSKDSQDRSSRSTICFVKKMKEXAMPRLTKEDIKPVWLSVDFPNWRMDEGDEEMELAH 120
OY      121 VEHYAELLKKVST 133
Db      121 VEHYAELMHST 133

RESULT 4
OY9D7V0 09D7V0 PRELIMINARY; PRT; 160 AA.
AC      09D7V0;
DT      01-JUN-2001 (TREMblrel. 17, Created)
DT      01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT      01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE      5730442A20RIK protein.
GN      TEBP OR 5730442A20RIK.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=STOMACH;
RX      MEDLINE=21085660; PubMed=11217851;
RA      Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA      Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA      Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA      Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA      Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA      Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

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RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE-EMBRYONIC STEM CELLS;
RX MEDLINE-21085660; Pubmed-11217851;
RA Kawai T., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hata A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kodora K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
RA Knehl P., Lewis S., Matsuo Y., Nikido I., Pesole G., Queckenbush J.,
RA Schirral L.M., Staudli F., Suzuki R., Tomita M., Wanner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baladrelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita A., Gariboldi M.,
RA Gustinlich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombeerts P.,
RA Nordone P., Ring B., Ringwald T., Maadina T., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilmink L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsunki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690(2001).
EMBL: AK010636; BAB27080.1; -

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; Euxaryales; Violiflorae; Sciepiaceae; Eubryoniales; Rhamnales; Rhamnaceae

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OC eurosids II; Brassicales; Brassicaceae; Brassica...
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. TOPAZ;
RA Cordenev J.H.G., Jansen H.J., Hause G., Fiers M.A.,
RA van Lookeren Campagne M.M.;
RT "np23, the plant ortholog of mammalian p23, is upregulated during
RT microspore embryogenesis in Brassica napus.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF153128; AAC41763.1; -
SQ SEQUENCE 178 AA; 20096 MW; 216E6DA677FE46A CRC64;

Query Match 15.5%; Score 131.5; DB 10; Length 178;
Best Local Similarity 32.2%; Pred. No. 6.1e-05;
Matches 37; Conservative 25; Mismatches 48; Indels 5; Gaps 5;

QY 4 OHATLWDRPMYVMECEVSDSTDVHYLE-DHRTVSCKNADGVELYN-EIEFYAKVN 61
DB 3 RHPIVKNARSDWYIYELPDADVDKLEPEGKFFSATSASGASKTILEYDLDDSDVD 62
QY 62 SKDSODKRSRSITCFVKKMKKAVMPRLTKEDIK-PWLSVDENMDWEGDEE 115
DB 63 VNEKASVSSNSVYLVKKAESK-WNRRLTKPEGKHPIYLAVDMKWD-EDDED 115

RESULT 8
Q9VJX8 PRELIMINARY; PRT; 371 AA.
AC Q9VJX8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE CG9267 protein.
GN CG9267.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sulten G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Aghayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballev R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cateley S., Dahlke C., Davenport L.B., Davies P.,
RA de Paolis B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertlera S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheller F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

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RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveli J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003640; AAF5307.1; -
DR FlyBase; FBgn0032524; CG9267.
SQ SEQUENCE 371 AA; 43682 MW; C23D7394BDFC2968 CRC64;

Query Match 14.7%; Score 125; DB 5; Length 371;
Best Local Similarity 36.2%; Pred. No. 0.00062;
Matches 34; Conservative 13; Mismatches 37; Indels 10; Gaps 4;

QY 45 ADGVELYN-EIEFYAKVSKDSODKRSRSITCFVKKMKKAVMPRLTKEDIKPWLSVD 103
DB 47 ARGVAAYFELHFTALIDENATFVSDNKIELOIRK-LEPEWMPRLVATPQPHMLKID 105
QY 104 FDNMRDMEGDDEME-----LAHVEHYAELLKK 130
DB 106 FDRWRT-EDDVEVEKPRDVRDYEKEYADLOKR 138

RESULT 9
Q8SYT0 PRELIMINARY; PRT; 371 AA.
AC Q8SYT0;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE RE57556P.
GN CG9267.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nuncio J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY071533; AAL49155.1; -
SQ SEQUENCE 371 AA; 43622 MW; C228939B5DE62968 CRC64;

Query Match 14.7%; Score 125; DB 5; Length 371;
Best Local Similarity 36.2%; Pred. No. 0.00062;
Matches 34; Conservative 13; Mismatches 37; Indels 10; Gaps 4;

QY 45 ADGVELYN-EIEFYAKVSKDSODKRSRSITCFVKKMKKAVMPRLTKEDIKPWLSVD 103
DB 47 ARGVAAYFELHFTALIDENATFVSDNKIELOIRK-LEPEWMPRLVATPQPHMLKID 105
QY 104 FDNMRDMEGDDEME-----LAHVEHYAELLKK 130
DB 106 FDRWRT-EDDVEVEKPRDVRDYEKEYADLOKR 138

RESULT 10
Q09003 PRELIMINARY; PRT; 190 AA.
AC Q09003;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

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DE B-IND1 protein (Fragment).
 GN HSPC121 OR B-IND1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 RX NCBI_TaxID=10090;
 RP [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=20286798; PubMed=10747961;
 RA Courilleau D., Chastre E., Sabbah M., Redeuilh G., Afifi A., Meister J.,
 RT "B-Ind1, a novel mediator of Rac1 signalling cloned from sodium
 butyrate-treated fibroblasts."
 RL J. Biol. Chem. 275:17344-17348(2000).
 DR EMBL: 297207; CAB10097.2;
 FT MGD; MG1:1889341; Hspc121.
 SQ SEQUENCE 190 AA; 22674 MW; 6499729F1C2FA549 CRC64;

Query Match 14.4%; Score 122; DB 11; Length 190;
 Best Local Similarity 30.2%; Pred. No. 0.00053;

Matches 39; Conservative 25; Mismatches 57; Indels 8; Gaps 6;

OY 10 WDRPMTVMFMEFCVSDTDVHLIEDHRIYVSC--NADGVELYN-EIEFYAKNSKDSQ 66
 DB 12 WAQRHRELYRVELSDYQNPASTITDVLHFKAGHGKGNVTEHLEFDLVKPEPAY 71
 OY 67 DKRSSITCFVRKWKKEKVAWPRLTKEIKPVLVDNMRDWDGEMELAHVEHYAE 126
 DB 72 -RLTOROVNTVQK-KQSHWMERLTKEKRPFLAPDFRDL-ESDAEMLRKKE--E 126
 OY 127 LKKVSTKR 135
 DB 127 RLRKRLER 135

RESULT 11

O9FT78 PRELIMINARY; PRT; 241 AA.

AC 09FT78;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE P23 co-chaperone.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 RX NCBI_TaxID=3702;
 RP [1]
 RN SEQUENCE FROM N.A.
 RA Bowra S.;
 RT "A plant p23: the missing link suggesting glucocorticoid receptors
 exist in plants."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A1297951; CAC16575.1;
 SQ SEQUENCE 241 AA; 25455 MW; 90989FE9550BDC3D CRC64;

Query Match 14.3%; Score 121; DB 10; Length 241;
 Best Local Similarity 27.6%; Pred. No. 0.00088;

Matches 35; Conservative 25; Mismatches 57; Indels 10; Gaps 5;

OY 4 OHARTLWDRPMYVMEFCVSDTDVHLIEDHRIY-FSCKNADGVELYN-EIEFYAKVN 61
 DB 3 RHPEVKWAETTEKIFLYVLADTKDTKYNLDPEGVFDSAKVGPNHYELKLELADKVN 62
 OY 62 SKDSQDKRSSRSTCFVRKWKKEKVAWPRLTKEIKPVLVDNMRDWDGDE-----E 115
 DB 63 VEESKINIGERSIFCIIEK-AEPRKMKLLRKRPYVKVDMKWD-EDDEGSAGAAD 120
 OY 116 MELAHVE 122
 DB 121 MDMA GME 127

RESULT 12

O81288 PRELIMINARY; PRT; 262 AA.

AC O81288;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)
 DE T14P8.5 protein.
 GN T14P8.5 OR A74G02450.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 RX NCBI_TaxID=3702;
 RP [1]
 RN SEQUENCE FROM N.A.
 RA STRAIN=CV. COLUMBIA;
 RA WASHU;
 RT "The A. thaliana Genome Sequencing Project."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Kalicki J., Elliott G., Cloud J.;
 RT "The sequence of A. thaliana T14P8."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RN [13]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Waterston R.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [14]
 RP SEQUENCE FROM N.A.
 RA Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [15]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF069238; AAC19287.1;
 DR EMBL: AL161494; CAB80738.1;
 KW Hypothetical protein.
 SQ SEQUENCE 262 AA; 27944 MW; 67BBP89EEF6625D6 CRC64;

Query Match 14.3%; Score 121; DB 10; Length 262;
 Best Local Similarity 27.6%; Pred. No. 0.00098;

Matches 35; Conservative 25; Mismatches 57; Indels 10; Gaps 5;

OY 4 OHARTLWDRPMYVMEFCVSDTDVHLIEDHRIY-FSCKNADGVELYN-EIEFYAKVN 61
 DB 7 RHPEVKWAETTEKIFLYVLADTKDTKYNLDPEGVFDSAKVGPNHYELKLELADKVN 66
 OY 62 SKDSQDKRSSRSTCFVRKWKKEKVAWPRLTKEIKPVLVDNMRDWDGDE-----E 115
 DB 67 VEESKINIGERSIFCIIEK-AEPRKMKLLRKRPYVKVDMKWD-EDDEGSAGAAD 124
 OY 116 MELAHVE 122
 DB 125 MDMA GME 131
 RESULT 13
 O8X041 PRELIMINARY; PRT; 216 AA.
 AC O8X041;
 DT 01-MAR-2002 (TREMblrel. 20, Created)
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Related to Hsp90 associated co-chaperone.
 GN BIK1.180.
 OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.

OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hohelsel J., Brandt P., Fartmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Manhaupt G.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL669998; CAD21185.1; -
 SQ SEQUENCE 216 AA; 23599 MW; 861F66CF350A61BF CRC64;

Query Match 13.8%; Score 117; DB 3; Length 216;
 Best Local Similarity 32.1%; Pred. No. 0.0019;
 Matches 35; Conservative 26; Mismatches 40; Indels 8; Gaps 5;

OY 16 YVFMCEVED--STDVHVLIEDHRIYFSCKNADGVLYN-EIEFYAKVNSKDSQDKRSSR 72
 Db 24 FYLTISVPDVPTSNLKLDPGLTGTSHSDTLKRTYHVELEFYAIDPMAAQVHHTAR 83
 OY 73 SITCFVRKKEKVA--WPRLTKEIDIKPVMLSYDFDNMRDMEGDEEMELAE 119
 Db 84 DVEMLIRK-KEIDAHYPRLLKEPKVHFLKTDFFDKWD--EDEQHFAA 129

RESULT 14

O96712 PRELIMINARY; PRT; 362 AA.

AC O96712:
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE CDNA FLJ14515 fis, clone NRZRM1000800, weakly similar to Mus
 DE musculus partial B-IND1 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Wagatsuma M., Hosokiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murekami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y.,
 RA Ninomiya K., Iwayanagi T.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK027421; BAB55101.1; -
 SQ SEQUENCE 362 AA; 43158 MW; EB371D668DDCCF075 CRC64;

Query Match 13.5%; Score 115; DB 4; Length 362;
 Best Local Similarity 29.6%; Pred. No. 0.0054;
 Matches 37; Conservative 24; Mismatches 56; Indels 8; Gaps 5;

OY 10 WYDRPMYVMEFCVEDSTDVHVLIEDHRIYFSCKNADGVLYN-EIEFYAKVNSKDSQ 66
 Db 12 WAOHRHELTLRVELSDVQNPALSTENVLHFKAQ-GHGAAGDNYEFHLFDLVKPEPV 70
 OY 67 DKRSSRSTICFYVRKKEKVAWPRLTKEIDIKPVMLSYDFDNMRDMEGDEEMELAEVHYAE 126
 Db 71 YKLTQGVNITVOK-KVSQWMERLTQEKRRPLFLAPDFRMLD-ESDAEMELRAKEE--E 126
 OY 127 LKKV 131
 Db 127 LKKV 131

RESULT 15

O9NOA7
 ID O9NOA7 PRELIMINARY; PRT; 370 AA.

AC O9NOA7:
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE B-ind1 protein.
 GN B-IND1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20298798; PubMed=10747961;
 RA Courtilleau D., Chastre E., Sabbah M., Redeuilh G., Affi A., Mester J.;
 RT "B-ind1, a novel mediator of Rac1 signalling cloned from sodium
 butyrate-treated fibroblasts."
 RL J. Biol. Chem. 275:17344-17348(2000).
 DR EMBL: AJ271091; CAB69070.1; -
 SQ SEQUENCE 370 AA; 43543 MW; 2D1E8ED1658BF00 CRC64;

Query Match 13.5%; Score 115; DB 4; Length 370;
 Best Local Similarity 30.4%; Pred. No. 0.0056;
 Matches 38; Conservative 23; Mismatches 56; Indels 8; Gaps 6;

OY 10 WYDRPMYVMEFCVEDSTDVHVLIEDHRIYFSC--NADGVLYN-EIEFYAKVNSKDSQ 66
 Db 12 WAOHRHELTLRVELSDVQNPALSTENVLHFKAQGHGAAGDNYEFHLFDLVKPEPV 71
 OY 67 DKRSSRSTICFYVRKKEKVAWPRLTKEIDIKPVMLSYDFDNMRDMEGDEEMELAEVHYAE 126
 Db 72 -KLTQGVNITVOK-KVSQWMERLTQEKRRPLFLAPDFRMLD-ESDAEMELRAKEE--E 126
 OY 127 LKKV 131
 Db 127 LKKV 131

Search completed: March 20, 2003, 05:20:07
 Job time : 80 secs